

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

-Run on: June 10, 2006, 05:36:37 ; Search time 16 Seconds
(without alignments)
272.619 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIESTGDYFLLCDAEG.....TQECFIQAKLSPOQDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 64916 seqs, 12643201 residues

Total number of hits satisfying chosen parameters: 64916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /EMC_Celerra_SID83/ptodata/1/pubpaa/US09_NEW_PUB.pap:
2: /EMC_Celerra_SID83/ptodata/1/pubpaa/US06_NEW_PUB.pap:
3: /EMC_Celerra_SID83/ptodata/1/pubpaa/US07_NEW_PUB.pap:
4: /EMC_Celerra_SID83/ptodata/1/pubpaa/US08_NEW_PUB.pap:
5: /EMC_Celerra_SID83/ptodata/1/pubpaa/PCT_NEW_PUB.pap:
6: /EMC_Celerra_SID83/ptodata/1/pubpaa/US10_NEW_PUB.pap:
7: /EMC_Celerra_SID83/ptodata/1/pubpaa/US11_NEW_PUB.pap:
8: /EMC_Celerra_SID83/ptodata/1/pubpaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498.5	27.5	403	US-10-505-928-203	Sequence 203, App
2	108.5	6.0	1836	US-11-313-450-8	Sequence 8, Appli
3	102.5	5.6	364	US-11-293-697-4612	Sequence 4612, Ap
4	100	5.5	360	US-11-242-111-19	Sequence 19, Appl
5	97.5	5.4	344	US-10-953-349-5324	Sequence 5324, Ap
6	97.5	5.4	419	US-10-953-349-5323	Sequence 5323, Ap
7	97.5	5.4	513	US-10-953-349-5322	Sequence 5322, Ap
8	97.5	5.4	2005	US-10-501-814-3	Sequence 3, Appli
9	97.5	5.4	2005	US-11-263-326-131	Sequence 131, App
10	97.5	5.4	2005	US-11-263-326-132	Sequence 132, App
11	97.5	5.4	2005	US-11-263-326-175	Sequence 175, App
12	97.5	5.4	2005	US-11-263-326-176	Sequence 176, App
13	97.5	5.4	2005	US-11-263-326-177	Sequence 177, App
14	97.5	5.4	2005	US-11-263-326-178	Sequence 178, App
15	97.5	5.4	2005	US-11-263-326-179	Sequence 179, App
16	97.5	5.4	2005	US-11-313-450-4	Sequence 4, Appli
17	96.5	5.3	2005	US-11-263-326-133	Sequence 133, App
18	96	5.3	1980	US-11-263-326-128	Sequence 128, App
19	96	5.3	1980	US-11-263-326-134	Sequence 134, App
20	96	5.3	1980	US-11-313-450-12	Sequence 12, Appl
21	93.5	5.1	402	US-10-471-571A-5294	Sequence 5294, Ap
22	93.5	5.1	2016	US-11-313-450-10	Sequence 10, Appl
23	92.5	5.1	469	US-10-471-571A-5254	Sequence 5254, Ap
24	92	5.1	2009	US-11-263-326-172	Sequence 172, App
25	91.5	5.0	306	US-10-953-349-38124	Sequence 38124, A

26 91.5 5.0 308 6 US-10-953-349-38123 Sequence 38123, A
27 91.5 5.0 337 6 US-10-953-349-38122 Sequence 38122, A
28 91 5.0 444 6 US-10-471-571A-2436 Sequence 2436, Ap
29 91 5.0 1795 7 US-11-263-326-124 Sequence 124, App
30 91 5.0 1855 7 US-11-263-326-125 Sequence 125, App
31 91 5.0 1891 7 US-11-263-326-173 Sequence 173, App
32 91 5.0 1977 7 US-11-251-465-24 Sequence 24, Appl
33 91 5.0 1977 7 US-11-313-450-14 Sequence 14, Appl
34 91 5.0 1998 7 US-11-313-450-2 Sequence 2, Appli
35 91 5.0 2009 7 US-11-263-326-4 Sequence 4, Appli
36 91 5.0 2009 7 US-11-263-326-10 Sequence 10, Appl
37 91 5.0 2009 7 US-11-263-326-12 Sequence 12, Appl
38 91 5.0 2009 7 US-11-263-326-121 Sequence 121, App
39 91 5.0 2009 7 US-11-263-326-122 Sequence 122, App
40 91 5.0 2009 7 US-11-263-326-126 Sequence 126, App
41 91 5.0 2009 7 US-11-263-326-127 Sequence 127, App
42 91 5.0 2009 7 US-11-263-326-167 Sequence 167, App
43 91 5.0 2009 7 US-11-263-326-168 Sequence 168, App
44 91 5.0 2009 7 US-11-263-326-169 Sequence 169, App
45 91 5.0 2009 7 US-11-263-326-169 Sequence 169, App

ALIGNMENTS

RESULT 1

US-10-505-928-203
; Sequence 203, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178 US/10/505,928
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-203

Query Match 27.5%; Score 498.5; DB 6; Length 403;
Best Local Similarity 35.8%; Pred. No. 1.4e-38;
Matches 112; Conservative 68; Mismatches 120; Indels 13; Gaps 7;

QY 12 YFLCDAEGPAGIILLESAILGIVVITLLALLAFLLMRKIODCSQNVLPQLLFLLSVL 71
Db 45 YVSLCDLDAIWGIVVEAVAGALITLLMLLILVRLPFKEKEKSPVGLHFLFLGTL 104
QY 72 GLFGAFATIIELNQTAPVRYFLGVLFCALCFSCLLAHASNLVLR-VCVSFSWTTIL 130
Db 105 GLFGATFATIIQEDETICSVRRFLGVLFCALCFSCLLSOAWRVRLRHGTGTGAGW-QLV 163
QY 131 CIAIGCSLLQIIATEYVTLINTRGMFMVNMTPCQLN-VDFVLLVYVFLMALTFVSK 189
Db 164 GLALCLMLVQVIAVEWLVLTRD---TRPACAYEPMDVFWALYDMVLLVVTGLAL 219
QY 190 ATFCGPGCNKQKGRILFITVLFSSIIIVVWLSMLLRGNPQFQPCQWDDPVVCIALVTN 249
Db 220 FTLCGKFRKWLNGAFLLITAFSLVLIWVAMTMYLFGNVKLQGGDAWNPDLTALTAAS 279
QY 250 ANVFLLLYIVPEL-CILYRSCRCQCPLOGNACPVYAYQHSFQVENCLESRDSDGA--- 305
Db 280 GWVFWIFRAIPEIHCTLLPALQENTPNYPTDSQPRMRETAFE-EDVQLPRAYMENKAFSM 338
QY 306 -EEDVALTSYGTP 317
Db 339 DEHNAALRTAGFP 351

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 05:35:42 ; Search time 178 seconds
(without alignments)
897.804 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIESTGDFLLCDAEG.....TQECFIPQAKLSPOODAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pgp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pgp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pgp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pgp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pgp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pgp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1816	100.0	345	4	US-10-225-567A-619
2	1816	100.0	345	4	US-10-600-816-4
3	1816	100.0	345	5	US-10-500-428-2
4	1816	100.0	345	5	US-10-501-841-56
5	1816	100.0	583	5	US-10-505-486-63
6	1809	99.6	345	4	US-10-467-252-8
7	1797.5	99.0	362	4	US-10-182-822A-14
8	1570.5	86.5	323	4	US-10-343-650A-2
9	1570	86.5	300	4	US-10-467-252-9
10	1570	86.5	317	4	US-10-276-774-2644
11	1318	72.6	300	4	US-10-600-816-5
12	1318	72.6	300	5	US-10-500-428-4
13	1213	66.8	229	4	US-10-029-386-34096
14	727.5	40.1	347	3	US-09-866-050A-326
15	727.5	40.1	357	4	US-10-176-847-60
16	727.5	40.1	357	4	US-10-225-567A-454
17	727.5	40.1	357	4	US-10-224-289-4
18	727.5	40.1	357	4	US-10-295-027-620
19	727.5	40.1	357	4	US-10-600-816-3
20	727.5	40.1	357	4	US-10-600-816-17
21	727.5	40.1	357	4	US-10-600-816-20
22	727.5	40.1	357	4	US-10-600-816-21
23	727.5	40.1	357	5	US-10-935-190-21
24	727.5	40.1	357	5	US-10-936-626-118
25	727.5	40.1	357	5	US-10-936-626-142
26	727.5	40.1	357	5	US-10-938-061-118
27	727.5	40.1	357	5	US-10-938-061-142

28	727.5	40.1	357	5	US-10-510-507-1	Sequence 1, Appli
29	727.5	40.1	357	6	US-11-080-991-60	Sequence 60, Appl
30	727.5	40.1	357	6	US-11-169-041-159	Sequence 159, App
31	727.5	40.1	409	4	US-10-284-049-3009	Sequence 3009, Ap
32	727.5	40.1	595	5	US-10-505-486-94	Sequence 94, Appli
33	726.5	40.0	357	4	US-10-600-816-8	Sequence 8, Appli
34	725.5	40.0	342	4	US-10-224-289-10	Sequence 10, Appl
35	725.5	40.0	357	4	US-10-600-816-9	Sequence 9, Appli
36	723.5	39.8	357	4	US-10-600-816-19	Sequence 19, Appl
37	687.5	37.9	313	3	US-09-864-761-35804	Sequence 35804, A
38	524.5	28.9	400	4	US-10-097-065-146	Sequence 146, App
39	524.5	28.9	400	4	US-10-372-876-146	Sequence 146, App
40	523.5	28.8	401	3	US-09-871-874-11	Sequence 11, Appl
41	523.5	28.8	446	3	US-09-871-874-10	Sequence 10, Appl
42	521.5	28.7	441	3	US-09-871-874-21	Sequence 21, Appl
43	521.5	28.7	441	3	US-09-895-686-1	Sequence 1, Appli
44	521.5	28.7	451	3	US-09-871-874-9	Sequence 9, Appli
45	521.5	28.7	451	3	US-09-871-874-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-225-567A-619
; Sequence 619, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 619
; TYPE: PRT
; LENGTH: 345
; ORGANISM: Homo sapiens
US-10-225-567A-619

Query Match	100.0%	Score 1816;	DB 4;	Length 345;
Best Local Similarity	100.0%	Pred. No. 3.2e-154;		
Matches	345;	Conservative	0;	Mismatches
		Indels	0;	Gaps
Qy	1	MYKDCIESTGDFLLCDAEGPWGIIIESAILGIVVTILLALLAFLLMRKIQDCSQNNVL	60	
Db	1	MYKDCIESTGDFLLCDAEGPWGIIIESAILGIVVTILLALLAFLLMRKIQDCSQNNVL	60	
Qy	61	PTOLLFLLSVGLFGIAFAFIHNLQOTAPRVYFLFGVLFALCFSCLLAHASNLVKLVRG	120	
Db	61	PTOLLFLLSVGLFGIAFAFIHNLQOTAPRVYFLFGVLFALCFSCLLAHASNLVKLVRG	120	
Qy	121	CVSFSWTTILCIAIGCSLLQIIATIEYVTLIMTRGMFMVNMTPCOLNDFVLLVYVFL	180	
Db	121	CVSFSWTTILCIAIGCSLLQIIATIEYVTLIMTRGMFMVNMTPCOLNDFVLLVYVFL	180	
Qy	181	MALTFPVSKATCGPCENKQHGRLIFITVLSIIIIWVWISMLLKGPNQFQPOQWDDP	240	
Db	181	MALTFPVSKATCGPCENKQHGRLIFITVLSIIIIWVWISMLLKGPNQFQPOQWDDP	240	
Qy	241	VVCIALVTWVFLLYIYVPELCILYRSCQECPLQGNACPVYAYOHSFOVENQELSRAR	300	
Db	241	VVCIALVTWVFLLYIYVPELCILYRSCQECPLQGNACPVYAYOHSFOVENQELSRAR	300	
Qy	301	DSGAEEDVALTSYGTPIQPTVDPQECFIPQAKLSPOODAGGV	345	
Db	301	DSGAEEDVALTSYGTPIQPTVDPQECFIPQAKLSPOODAGGV	345	

GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

```

~ Run on: June 10, 2006, 05:34:57 ; Search time 50 Seconds
          (without alignments)
          603.961 Million cell v

```

Title: US-10-500-428-2
Perfect score: 1816
Sequence: 1 MYKDCIESTGDYFLLCDAEG.....TOECFIPQAKLSPQDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: .650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

```

Database :
Issued Patents_AA.*
1: /EMC_Celerra SIDS3/ptodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra SIDS3/ptodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra SIDS3/ptodata/2/iaa/H_COMB.pep.*
5: /EMC_Celerra SIDS3/ptodata/2/iaa/PCTRUS COMB.pep.*
6: /EMC_Celerra SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC_Celerra SIDS3/ptodata/2/iaa/backfiles1.pep.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	727.5	40.1	347	2	US-09-188-930-326	Sequence 326, Appl
2	727.5	40.1	347	2	US-09-312-283C-326	Sequence 326, Appl
3	727.5	40.1	357	2	US-09-949-016-6443	Sequence 6443, Ap
4	727.5	40.1	390	2	US-09-949-016-9484	Sequence 9484, Ap
5	213	11.7	68	2	US-09-188-930-123	Sequence 123, App
6	213	11.7	68	2	US-09-312-283C-123	Sequence 123, App
7	183	10.1	256	2	US-09-964-956-85	Sequence 85, Appl
8	164.5	9.1	1027	2	US-09-162-021B-2	Sequence 2, Appli
9	164.5	9.1	1027	2	US-10-268-051-8	Sequence 8, Appli
10	164.5	9.1	1027	2	US-10-125-772-2	Sequence 2, Appli
11	164.5	9.1	1027	2	US-10-125-778-2	Sequence 2, Appli
12	164.5	9.1	1027	2	US-10-125-792-2	Sequence 2, Appli
13	163	9.0	863	2	US-09-619-353-14	Sequence 14, Appl
14	159.5	8.8	1078	1	US-08-485-588-7	Sequence 7, Appli
15	159.5	8.8	1078	1	US-08-484-565-7	Sequence 7, Appli
16	159.5	8.8	1078	1	US-08-480-751-7	Sequence 7, Appli
17	159.5	8.8	1078	1	US-08-943-986-7	Sequence 7, Appli
18	159.5	8.8	1078	2	US-08-353-784-7	Sequence 7, Appli
19	159.5	8.8	1078	2	US-08-484-719B-7	Sequence 7, Appli
20	159.5	8.8	1078	2	US-08-484-159-7	Sequence 7, Appli
21	159.5	8.8	1078	2	US-10-125-772-28	Sequence 28, Appl
22	159.5	8.8	1078	2	US-10-125-778-28	Sequence 28, Appl
23	159.5	8.8	1078	2	US-10-125-792-28	Sequence 28, Appl
24	159.5	8.8	1088	1	US-08-485-588-6	Sequence 6, Appli
25	159.5	8.8	1088	1	US-08-484-565-6	Sequence 6, Appli
26	159.5	8.8	1088	1	US-08-480-751-6	Sequence 6, Appli

ALIGNMENTS

```

RESULT 1
US-09-188-930-326
; Sequence 326, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 326
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-326

```

Query Match	40.1%;	Score	727.5;	DB 2;	Length	347;			
Best Local Similarity	45.7%;	Pred. No.	1.4e-62;						
Matches	154;	Conservative	55;	Mismatches	117;	Indels	11;	Gaps	6;
QY	12	YFLLCDAGPGWIGIILESAILGIVVTIILLALLAPFLMRKIQCSQMNVLPTQLFLLSVL	71						
Db	7	YYRLCDKAEAWGIVLETVATAGVTVSAPMLTLPILVCKVQDSNRRKMLPTQFLFLGVL	66						
QY	72	GLFLGAPAFIIELNQOTAPVRVFLFGVLPALCFSCLLAHASNVLKLVRCGVCSFWTILC	131						
Db	67	GIFGTFAPFIILGDSTGTPREFFLGILFSICFSCLLAHAVSLTKLVGRKPLSLLVILG	126						
QY	132	TAIGCSLLQIIATISVYVTLIMTRG--MRFVNMTPCQLNVDFVLLVYVFLMALTFVSK	189						
Db	127	LAVGSLVDQVIAEYIVLTWNRTNVNVFSELSAPRNEDFVLLLTLYVFLMALTFMLSS	186						
QY	190	ATFCGPCENKQHGRLIFITVLFSTIIIVVWVLSMLLRGNPQORQORQWDPPVCIALVTN	249						
Db	187	FTFCGSFTGWRKHGAHIYLTMLLSIAIWWAITLML--PDFDR--RWDOTILUSSALAN	242						
QY	250	AWVFLLLYIVPELCILYRSCR--QECPLQGNACPVTAYQHSFOVENELSRARSDGAE--	307						
Db	243	GWVFLLAYVSEFWLLTKQRNPMDYVEDAFCKPOLVKSYGVENRAYSQEETITQGFET	302						
QY	308	-DVALTSGTPIQPTVDPTQECFIPQAKL--SPOOD	341						

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 05:26:22 ; Search time 296 Seconds
(without alignments)
1078.143 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDIESTGDFLLCDABE.....TQECFIPQAKLSPPQAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	345	1	GPC5D_HUMAN
2	1816	100.0	345	2	Q3KNV3_HUMAN
3	1494	82.3	344	1	GPC5D_MOUSE
4	1494	82.3	344	2	Q3UUY8_MOUSE
5	737.5	40.6	357	2	Q6P25_XENLA
6	727.5	40.1	357	1	RAI3_HUMAN
7	719.5	39.6	357	2	Q3MHQ6_BOVIN
8	700	38.5	356	1	RAI3_MOUSE
9	549.5	30.3	408	2	Q5M7K5_XENTR
10	540	29.7	468	2	Q2YDQ0_BOVIN
11	532.5	29.3	440	1	GPC5C_MOUSE
12	531.5	29.3	457	2	Q3KRC4_RAT
13	523.5	28.8	452	2	Q53GM2_HUMAN
14	521.5	28.7	441	1	GPC5C_HUMAN
15	521.5	28.7	486	2	Q2NL85_HUMAN
16	504	27.8	432	2	Q5M7Q6_XENTR
17	498.5	27.5	403	1	GPC5B_HUMAN
18	497.5	27.4	410	1	GPC5B_MOUSE
19	496.5	27.3	403	2	Q5R3B9_PONPY
20	479.5	26.4	403	2	Q5R6C3_PONPY
21	443	24.4	393	2	Q4RMJ3_TETNG
22	424	23.3	353	2	Q4SGJ6_TETNG
23	398.5	21.9	349	2	Q4S8I2_TETNG
24	341	18.8	537	2	Q4RXZ7_TETNG
25	300.5	16.5	188	2	Q5RK14_RAT
26	260.5	14.3	262	2	Q9JMF0_MOUSE
27	168.5	9.3	893	1	BOSS_DROVI
28	166.5	9.2	1404	2	Q20073_CABEL
29	164.5	9.1	1027	2	Q8J104_SQUAC
30	164	9.0	867	1	GPC6A_BRARE
31	162.5	8.9	896	1	BOSS_DROME

RESULT 1

ID	GPC5D_HUMAN	STANDARD;	PRT;	345 AA.
AC	Q9NZD1; Q725J9; Q8TDS6;			
DT	13-APR-2004, integrated into UniProtKB/Swiss-Prot.			
DT	01-OCT-2000, sequence version 1.			
DT	07-FEB-2006, entry version 26.			
DE	G-protein coupled receptor family C group 5 member D.			
GN	Name=GPC5D;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1), TISSUE SPECIFICITY, SUBCELLULAR			
RP	LOCATION, AND INDUCTION.			
RC	TISSUE=Testis;			
RX	MEDLINE=21210966; PubMed=11311935;			
RA	Braeuner-Osborne H., Jensen A.A., Sheppard P.O., Brodin B.,			
RA	Krogsgaard-Larsen P., O'Hara P.;			
RT	"Cloning and characterization of a human orphan family C G-protein			
RT	coupled receptor GPRC5D.";			
RL	Biochim. Biophys. Acta 1518:237-248 (2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 2).			
RC	TISSUE=Skin;			
RA	Inoue S., Nanbu T., Shimomura T.;			
RT	"Characterization of GPRC5D, a member of RAIG family in hard			
RT	keratinized structures.";			
RN	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 3).			
RX	MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;			
RA	Takeda S., Kadowaki S., Haga T., Tokaesu H., Mitaku S.;			
RT	"Identification of G protein-coupled receptor genes from the human			
RL	genome sequence.";			
RN	FEBS Lett. 520:97-101 (2002).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 05:29:57 ; Search time 41 Seconds
(without alignments)
809.629 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIESTGDYFLLCDAEG.....TOECFIPQAKLSPOQDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	168.5	9.3	893	2 A47550	bride of sevenless
2	166.5	9.2	1099	2 T16283	hypothetical prote
3	165.5	9.1	896	2 S26740	gene boss protein
4	162.5	8.9	896	2 A36455	bride of sevenless
5	159.5	8.8	1078	2 A56715	calcium receptor (
6	159.5	8.8	1088	2 B56715	calcium receptor (
7	158.5	8.7	1085	2 S40476	Ca(2+)-sensing rec
8	147	8.1	1079	2 I59362	calcium/polyvalent
9	130	7.2	872	2 JH0561	metabotropic gluta
10	130	7.2	879	2 JH0562	metabotropic gluta
11	130	7.2	879	2 JH0562	metabotropic gluta
12	122	6.7	298	2 S15433	hypothetical prote
13	122	6.7	496	2 E82940	hypothetical prote
14	119	6.6	150	2 S43955	probable NADH2 deh
15	116.5	6.4	826	2 T28858	hypothetical prote
16	111	6.1	678	2 B71308	hypothetical prote
17	110	6.1	281	1 S26018	NADH2 dehydrogenas
18	110	6.1	635	1 A64162	cytochrome c-type
19	109.5	6.0	328	2 T11227	NADH2 dehydrogenas
20	109.5	6.0	1840	1 CHRTM1	sodium channel pro
21	109	6.0	288	2 S36954	cytochrome-c oxida
22	109	6.0	288	2 S36955	cytochrome-c oxida
23	108.5	6.0	1835	2 I54323	sodium channel alp
24	108.5	6.0	1836	2 I64893	sodium channel alp
25	108.5	6.0	1836	2 J06488	sodium channel alp
26	108.5	6.0	1836	2 I51964	sodium channel alp
27	108	5.9	445	2 E22845	hypothetical prote
28	108	5.9	871	2 A46742	metabotropic gluta
29	107.5	5.9	287	2 A25877	cytochrome-c oxida

ALIGNMENTS

RESULT 1

A47550

bride of sevenless precursor - fruit fly (Drosophila virilis)

N;Alternate names: boss

C;Species: Drosophila virilis

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: A47550

R;Hart, A.C.; Harrison, S.D.; Van Vactor Jr., D.L.; Rubin, G.M.; Zipursky, S.L.

Proc. Natl. Acad. Sci. U.S.A. 90, 5047-5051, 1993

A;Title: The interaction of bride of sevenless with sevenless is conserved between Drosophila and Drosophila

A;Reference number: A47550; MUID:93281693; PMID:8506350

A;Accession: A47550

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-893 <HAR>

A;Cross-references: UNIPROT:Q24738; UNIPARC:UPI0000126A67; GB:L08132; NID:g290215; PII

C;Genetics:

A;Gene: FlyBase:Dvir/boss

A;Cross-references: FlyBase:FBgn0013105

A;Introns: 14/3; 175/3; 324/3; 808/3

C;Keywords: transmembrane protein

Query Match 9.3%; Score 168.5; DB 2; Length 893;

Best Local Similarity 21.2%; Pred. No. 3.3e-06;

Matches 84; Conservative 70; Mismatches 116; Indels 127; Gaps 20;

QY 4 DCIESTGD---YFLCDAEGP--WGIIIE-----SLAILGIVVTILLALLFLMRKI 51

Db 497 NCQFTAGENRRYPFFLDGESVMPFRIKLDTWATGLTAAILGLIAT-LAILVFIVRISL 555

QY 52 QDCSQNNVLTQLFLSLVLGLAFATIE-----LNQQTAPVRYF 94

Db 556 GDVFEGNPV-TSILLLLILVFCSPFMSYVGEORNSHVTFEDVHTLN-TLCGVRF 613

QY 95 LFGVLFCALCFSCILAHASNLVKL-----VRGCVSFSWTILC-----IAIGCSLLQ 140

Db 614 IMTLVCFVFSLLLCRAVMLASIGSEGGFLSHVNGYIQ-----AIICVLSVFVQVMSVOL 669

QY 141 IIII---ATEYVTLIMTRGMFMVMTPCQ-----LNVDVFLVLLVFLMALTF 186

Db 670 LVVMHLASSVS-----CENIYVGRWLGLAYDFLL-----CSLVSIVPF 711

QY 187 VSKATPCGCENKQGRILIFTVPSIIIVVWISMLLRGNPQFORQPDQVPCIAL 246

Db 712 IYRSQ-----RNYRE-GILIVIGAVLLIISWVIALSMFGD-----EWRDAAPLGM 758

QY 247 VTNVAVFLLYIVPELCILYRSCRCQPCLOGNACPTAYQHSFOVENQELSRARDSDGAE 306

Db 759 QASGAVLVGIIIPRTFLVRG-----IERSDIAQALPS--- 792

QY 307 EDVALTS--YGTPIQPTQVDPTEQCFIPQAKLSPOOD 341

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2006, 05:26:07 ; Search time 199 Seconds
(without alignments)
792.662 Million cell updates/sec

Title: US-10-500-428-2

Perfect score: 1816

Sequence: 1 MYKDCIBSTGDFYLLCDAEG.....TOECFIPQAKLSPOQDAGGV 345

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*
- 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	1816	100.0	345	ABP81722	Human G p
2	1816	100.0	345	ADB80899	Anorexia
3	1816	100.0	345	ADD67579	Human Ly1
4	1816	100.0	345	ADO29466	Human GPC
5	1816	100.0	583	ADF70440	Orphan re
6	1809	99.6	345	ABF71329	Human GCR
7	1804	99.3	345	ADS10857	Human the
8	1797.5	99.0	362	AAE06764	Human G-p
9	1570.5	86.5	323	AB691174	Human G-p
10	1570.5	86.5	323	ABP95596	Human GPC
11	1570	86.5	300	AB71330	Human GCR
12	1570	86.5	300	ADC98222	Human G p
13	1570	86.5	317	ABB12274	Human orp
14	1570	86.5	317	ADS12107	Human the
15	1318	72.6	300	ADB80901	Anorexia
16	1318	72.6	300	ADC98220	Mouse G p
17	1318	72.6	300	ADO29467	Mouse GPC
18	1213	66.8	229	ABO60462	Human gen
19	727.5	40.1	347	AA76071	Rat skin
20	727.5	40.1	347	AA856010	Skin cell
21	727.5	40.1	347	ABB72210	Human pro
22	727.5	40.1	352	ADI28547	Human GPC
23	727.5	40.1	352	ADI28461	Human GPC

24	727.5	40.1	357	4	AAB68891	Human REC
25	727.5	40.1	357	4	AAB93311	Human pro
26	727.5	40.1	357	6	ABR58569	Human can
27	727.5	40.1	357	6	ABJ37054	Human bre
28	727.5	40.1	357	6	ABR42649	Human GPC
29	727.5	40.1	357	6	ABP81984	Human G p
30	727.5	40.1	357	7	ADD93239	RAIG1. 1/
31	727.5	40.1	357	7	ADN39302	Cancer/an
32	727.5	40.1	357	8	ADI28460	Human GPC
33	727.5	40.1	357	8	ADO29632	Human GPC
34	727.5	40.1	357	8	ADR48222	Human ret
35	727.5	40.1	357	8	ABM81354	Tumour-as
36	727.5	40.1	357	8	ADU06613	Novel bro
37	727.5	40.1	357	9	AEA00166	Human TAT
38	727.5	40.1	357	9	AEA00190	Human TAT
39	727.5	40.1	357	9	AEA00686	Human TAT
40	727.5	40.1	357	9	AEA00710	Human TAT
41	727.5	40.1	357	9	AED47479	Retinoic
42	727.5	40.1	401	8	ADX97565	Pancreat
43	727.5	40.1	409	5	ABP41877	Human ova
44	727.5	40.1	595	7	ADF70471	Orphan re
45	726.5	40.0	357	8	ADI28535	Human GPC

ALIGNMENTS

RESULT 1

ABP81722
ID ABP81722 standard; protein; 345 AA.

XX AC ABP81722;

XX DT 04-MAR-2003 (first entry)

XX DE Human G protein-coupled receptor GPRC5D protein SEQ ID NO:619.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US050107.

XX PR 19-DEC-2000; 2000US-0257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burmer GC, Roush CL, Brown JP;

XX DR WPI; 2003-046718/04.

XX DR N-PSDB; ABZ42568.

XX KW New isolated antigenic peptides e.g., for G protein-coupled receptors
(GPCR), useful for diagnosing and designing drugs for treating conditions
in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
autoimmune diseases.

XX PS Disclosure; Fig 1; 523pp; English.